

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: November 3, 2005, 08:43:50 ; Search time 168 Seconds

(without alignments)
657.501 Million cell updates/sec

Title: US-10-813-549-1
Perfect score: 1380
MAISIKTPDIEKVRVAGRL.....CEILTIRKDDTIPAIISHDB 264

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

1: /cgmn_6/ptodata/1/pubpaal/US07_PUBCOMB.pep:*

2: /cgmn_6/ptodata/1/pubpaal/US06_PUBCOMB.pep:*

3: /cgmn_6/ptodata/1/pubpaal/US06_NEW_PUBCOMB.pep:*

4: /cgmn_6/ptodata/1/pubpaal/US07_NEW_PUBCOMB.pep:*

5: /cgmn_6/ptodata/1/pubpaal/US10_PUBCOMB.pep:*

6: /cgmn_6/ptodata/1/pubpaal/PTC15_PUBCOMB.pep:*

7: /cgmn_6/ptodata/1/pubpaal/US08_NEW_PUBCOMB.pep:*

8: /cgmn_6/ptodata/1/pubpaal/US08_PUBCOMB.pep:*

9: /cgmn_6/ptodata/1/pubpaal/US09_PUBCOMB.pep:*

10: /cgmn_6/ptodata/1/pubpaal/US09C_PUBCOMB.pep:*

11: /cgmn_6/ptodata/1/pubpaal/US10A_PUBCOMB.pep:*

12: /cgmn_6/ptodata/1/pubpaal/US10B_PUBCOMB.pep:*

13: /cgmn_6/ptodata/1/pubpaal/US10A_PUBCOMB.pep:*

14: /cgmn_6/ptodata/1/pubpaal/US10B_PUBCOMB.pep:*

15: /cgmn_6/ptodata/1/pubpaal/US10C_PUBCOMB.pep:*

16: /cgmn_6/ptodata/1/pubpaal/US10D_PUBCOMB.pep:*

17: /cgmn_6/ptodata/1/pubpaal/US10D_PUBCOMB.pep:*

18: /cgmn_6/ptodata/1/puppaal/US10_NEW_PUBCOMB.pep:*

19: /cgmn_6/ptodata/1/puppaal/US11_PUBCOMB.pep:*

20: /cgmn_6/ptodata/1/puppaal/US11_NEW_PUBCOMB.pep:*

21: /cgmn_6/ptodata/1/puppaal/US60_PUBCOMB.pep:*

22: /cgmn_6/ptodata/1/puppaal/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1
US-10-299-867-12 ; Sequence 12, Application US/10299867
; Publication No. US10030203405A1
; GENERAL INFORMATION:
; APPLICANT: Sympon, Carolyn J.
; APPLICANT: Aurora, Radeev
; APPLICANT: Dotson, Stanton B.
; APPLICANT: Frazier, Ronald B.
; APPLICANT: Woods, Cynthia L.
; APPLICANT: Zakeri, Hamideh
; APPLICANT: Zhou, Xianzhi
; TITLE OF INVENTION: Human methionine aminopeptidase type 3
; TITLE OF INVENTION: (MetAP-3)
; FILE REFERENCE: S03181-01-US
; CURRENT APPLICATION NUMBER: US/10/299-867
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: US 60/125,139
; PRIOR FILING DATE: 1999-03-11
; PRIORITY CLAIMS:
; PRIORITY DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 264
; TYPE: PRT
; ORGANISM: E. coli M_{et}AP
US-10-299-867-12
Query Match 100.0%; Score 1380; DB 15; Length 264;
Best Local Similarity 100.0%; Pred. No. 2.2e-133;
Matches 264; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Sequence 1, Appli
Sequence 12, Appli
Sequence 8, Appli
Sequence 31, Appli
Sequence 1, Appli
Sequence 9, Appli
Sequence 13, Appli
Sequence 121, Appli
Sequence 59, Appli
Sequence 61, Appli
Sequence 123, Appli
Sequence 10, Appli
1 MAISIKTPDIEKVRVAGRLAELVLEMPVYRPGVSTGELDRICNDYIVNBOHAVSACL 60

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OM protein - protein search, using SW model

Run on: November 3, 2005, 08:42:11 ; Search time 44 seconds

(without alignments)
 447,894 Million cell updates/sec

Title: US-10-813-549-1
 Perfect score: 1380
 Sequence: 1 MAISIKTPEDIKEMVAGRL. CELTIRKDDTIPAIISHDE 264

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5
 513545 seqs, 74649064 residues

Searched:

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/podata/1/iaa/5A_COMB.pep: *
 2: /cgn2_6/podata/1/iaa/5B_COMB.pep: *
 3: /cgn2_6/podata/1/iaa/6A_COMB.pep: *
 4: /cgn2_6/podata/1/iaa/6B_COMB.pep: *
 5: /cgn2_6/podata/1/iaa/PCTUS_COMB.pep: *
 6: /cgn2_6/podata/1/iaa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	1380	100	4	US-09-553-263B-12
2	1330	96	4	US-09-899-039A-12389
3	1086	78	4	US-09-543-681A-6596
4	910.5	66	4	US-09-553-263B-13
5	909.5	65	4	US-09-552-991A-0742
6	824.5	59	4	US-09-328-352-4434
7	799.5	57	4	US-09-440-236-2577
8	798	57	4	US-09-28-757-7575
9	739	53	4	US-09-352-991A-31271
10	701	50	4	US-09-443-681A-7847
11	682	49	4	US-09-566-056-2
12	669.5	48	4	US-09-533-263B-10
13	646	46	4	US-09-523-263B-11
14	614	44	4	US-09-523-263B-2
15	595.5	43	4	US-09-602-777A-36
16	583	42	4	US-09-523-263B-15
17	565	40	4	US-09-523-63B-14
18	559.5	40.5	4	US-09-223-263B-9
19	559.5	40.5	4	US-09-097-767-41600
20	556.5	40	3	US-09-97-906-4
21	552.5	40	4	US-09-902-540-12329
22	532.5	40	3	US-09-97-906-5
23	539	39.1	4	US-09-198-452A-1081
24	539	39.1	4	US-09-338-185A-1010
25	489.5	35.5	3	US-09-197-906-2
26	489.5	35.5	3	US-09-246-263B-8
27	473	34.3	4	US-09-523-263B-2

ALIGNMENTS

RESULT 1
 US-09-523-263B-12
 Sequence 12, Appl
 Patent No. 6638750

GENERAL INFORMATION:

APPLICANT: Aurora et al.

FILE REFERENCE: S03181-00-US

TITLE OF INVENTION: Methionine aminopeptidase type 3

CURRENT APPLICATION NUMBER: US/09/523, 263B

CURRENT FILING DATE: 2000-03-10

PRIOR APPLICATION NUMBER: 60/125, 139

PRIOR FILING DATE: 1999-03-11

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO: 12

LENGTH: 264

TYPE: PRT

ORGANISM: *E. coli* MetAP

US-09-523-263B-12

Query Match 100.0% ; Score 1380; DB 4; Length 264;
 Best Local Similarity 100.0%; Pred. No. 2. 4e-147;
 Matches 264; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAISIKTPEDIKEMVAGRLAEVLEMIEPVKPGVSTGELDRICNDYVNEOHAVSACL
 Db 1 MAISIKTPEDIKEMVAGRLAEVLEMIEPVKPGVSTGELDRICNDYVNEOHAVSACL 60
 QY 61 GHGHPKPSVCGISINEVCHGIPDDAKLKGODIVNDVTWIKDGFGDTSKQFIVGKPTI 120
 Db 61 GHGHPKPSVCGISINEVCHGIPDDAKLKGODIVNDVTWIKDGFGDTSKQFIVGKPTI 120
 QY 121 MGERLICRITQESLYALRMYKPGMIREGAIOKVEAEFSVWRYCGIGIGRGPHE 180
 Db 121 MGERLICRITQESLYALRMYKPGMIREGAIOKVEAEFSVWRYCGIGIGRGPHE 180
 QY 181 PQVLYHDSRTEINWVULKPGMFTIEPMVNAKGKEIRTMKGDTVKTQDLSAQYEHIV 240
 Db 181 PQVLYHDSRTEINWVULKPGMFTIEPMVNAKGKEIRTMKGDTVKTQDLSAQYEHIV 240
 QY 241 TDNGCEILTIRKDDTIPAIISHDE 264
 Db 241 TDNGCEILTIRKDDTIPAIISHDE 264

RESULT 2
 US-09-489-039A-12389
 ; Sequence 12389, Application US/09489039A
 ; Patent No. 6610356
 ; GENERAL INFORMATION:

Copyright (c) 1993 - 2005 Compugen Ltd.	GenCore version 5.1.6		
Run on: November 3, 2005, 08:30:15 ; search time 165 Seconds			
OM protein - protein search, using sw model			
Sequence: 1 MAISIKTPEDIKMRVAGL.....CEILTRKDTTIPAIISIDE 264	(without alignments)		
Scoring table: BLOSUM62	618.817 Million cell updates/sec		
Searched: 2105692 seqs, 386760381 residues			
Total number of hits satisfying chosen parameters: 2105692			
Minimum DB seq length: 0			
Maximum DB seq length: 200000000			
Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries:			
Database : A_Geneseq_16Dec04:*			
1: geneseqP1980s:*			
2: geneseqP1990s:*			
3: geneseqP2000s:*			
4: geneseqP2001s:*			
5: geneseqP2002s:*			
6: geneseqP2003as:*			
7: geneseqP2003bs:*			
8: geneseqP2004s:*			
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.			
SUMMARIES			
Result No.	Score	Query Match Length DB ID	Description
1	1380	100.0	264 1 ADP70096
2	1380	100.0	264 4 ADP29345
3	1380	100.0	264 7 ADG44839
4	1380	100.0	264 7 ADG25269
5	1380	100.0	264 7 ADG42853
6	1371	99.3	263 7 ADG25270
7	1330	96.4	281 7 ADG65872
8	1137.5	82.4	266 6 ADP67554
9	1086	78.7	268 7 ADP06311
10	910.5	66.0	268 7 ADG44840
11	910.5	66.0	268 7 ADG42854
12	910.5	66.0	268 7 ADG73413
13	909.5	65.9	261 7 ADG73351
14	909.5	65.9	261 7 ADG73353
15	909.5	65.9	285 7 ADP07196
16	904.5	63.5	268 7 ADG73415
17	824.5	59.7	286 6 ADG33147
18	799.5	57.9	268 8 ADP04891
19	798	57.8	264 6 ADP36289
20	739	53.6	303 7 ADP08252
21	701	50.8	265 7 ADP07562
22	682	49.4	264 2 ADW89276
23	669.5	48.5	253 7 ADG25265
24	669.5	48.5	253 7 ADG42851
253	669.5	48.5	
ALIGMENTS			
RESULT 1			
ID XX	AAP70096 standard; protein; 264 AA.		
AC XX	AAP70096;		
DT 09-APR-1991	(First entry)		
DE Met-aminopeptidase.			
XX	Met-aminopeptidase; antibody; plasmid PSYC1174.		
XX	Escherichia coli.		
XX			
PN XX	EP219237-A.		
PD XX	22-APR-1987.		
PR XX	19-SEP-1986;		
PR XX	20-SEP-1985;		
PR 06-MAY-1986;	85US-0077414.		
PR 06-MAY-1986;	86US-00860330.		
RA XX	(CETU) CERTUS CORP.		
PI XX	Benbasat A, Bauer KA, Chang S, Chang SY;		
XX	WPI; 1987-110172/16.		
DR N-PSDB; AAN70131.			
XX			
PT XX	N-terminal methionine free proteins prodn. - by using host transformed		
PT XX	with vector to express a methionine-amino-peptidase.		
PT XX	Disclosure; Fig 2; 20pp; English.		
XX			
CC	The enzyme (from E.coli) is encoded by the 1.2 kb insert of PSYC1174.		
CC	Proteins, esp. foreign proteins, lacking an N-terminal Met can be		
CC	produced in bacterial systems, esp. interleukin-2 or ricin A. Antibodies		
CC	to the enzyme are used for identifying such enzymes from various		
CC	microorganisms. The enzyme pref. hydrolyses the N-terminal Met from Met- Y		
CC	-Z (Tala, Pro, Ile or Gly, 2-amino acid) and does not hydrolyse		
CC	dipeptides		
XX			
SQ Sequence 264 AA;			
Query Match 100.0%; Score 1380; DB 1; Length 264;			
Best Local Similarity 100.0%; Pred. No. 3e-140;			
Matches 264; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			

OM protein - protein search, using SW model

Run on: November 3, 2005, 08:31:04 ; Search time 175 Seconds

(without alignments) 772,508 Million cell updates/sec

Title: US-10-813-549-1
Perfect score: 1380
Sequence: 1 MAISIKTPEDIEKMRVAGRL.....CEILTURKDDTIPATISHDE 264

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:

1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03;*
1: uniprot_sprot;*
2: uniprot_trembl;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	1380	100.0	264	1	AMPM_ECOLI	P07906 escherichia
2	1253	90.8	263	1	AMPM_SALTY	P10892 salmonella
3	1198	86.8	263	2	06677B	Q66718 yersinia ps
4	1195	86.6	263	2	082H67	Q8z167 yersinia pe
5	1158	83.9	264	2	06d8E4	Q6d8E4 eswilia car
6	1137.5	82.4	265	2	07N8P8	Q7N8P8 photorhabdu
7	946	82.4	267	2	09CNH2	Q9CNH2 pasteurella
8	937	67.9	264	1	AMPM_BUCAL	P57224 buchnera ap
9	934	67.7	268	2	07VP53	Q7VP53 haemophilus
10	919.5	66.6	260	2	0886P4	Q886P4 pseudomonas
11	919.5	66.3	264	2	07VR87	Q7VR87 candidatus
12	914.5	66.3	260	2	088M11	Q88M11 pseudomonas
13	910.5	66.0	268	1	AMPM_HAEIN	P44421 haemophilus
14	909.5	65.9	261	2	09hX71	Q9hX71 pseudomonas
15	902	65.4	251	1	AMPM_BUCAP	P8k3T1 buchnera ap
16	885.5	64.2	270	2	065S27	Q65S27 manneimia
17	881	63.8	258	2	083BV1	Q83BV1 coxiella bu
18	880.5	63.8	275	2	06LN23	Q6LN23 photobacter
19	878	63.6	258	2	08PMP9	Q8PMP9 xanthomonas
20	874	63.3	258	2	08PAU5	Q8PAU5 xanthomonas
21	853.5	61.8	259	2	07QMC0	Q7QMC0 anophelles g
22	853	61.8	258	2	087f52	Q87f52 xylella fast
23	852	61.7	259	2	09Pf33	Q9Pf33 xylella fast
24	852	61.7	263	2	08D2G1	Q8D2G1 wiggleswort
25	849.5	61.6	266	1	AMPM_BUCCP	Q84953 yersinia pe
26	843.5	61.1	265	1	Q8BCH7	Q8BCH7 pseudomonas
27	823.5	59.7	280	2	Q8KPV1	Q8KPV1 vibrio chol
28	804	58.3	272	2	Q82XJ5	Q82XJ5 nitrosomonas
29	798	57.8	271	2	Q62JG3	Q62JG3 burkhodella
30	798	57.8	271	2	Q63T11	Q63T11 burkhodella
31	796.5	57.7	261	2	Q66e99	Q66e99 yersinia ps

ALIGNMENTS

RESULT 1	AMPM_ECOLI	STANDARD;	PRT;	264 AA.
ID	AMPM_ECOLI			
AC	P07906;			
DT	01-AUG-1988 (Rel. 08, Created)			
DT	01-AUG-1988 (Rel. 08, Last sequence update)			
DE	25-JAN-2005 (Rel. 46, Last annotation update)			
GN	Methionine aminopeptidase (EC 3.4.11.18) (MAP)			
Name=map;				
GN	OrderedLocusNames=b0168, c0203, z0178, ECB0170, SF0158, S0161;			
GN	Escherichia coli, O6, Escherichia coli O17:H7, and			
RC	Shigella flexneri, Bacteriia; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia. [1]			
RC	Bacteriia; Proteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia coli 017:H7, and			
RC	SEQUENCE FROM N. A.			
RC	SPECIES=E.coli;			
RC	MEDLINE=81109088; PubMed=3027045;			
RC	Q7N8P8 photorhabdu			
RC	Q9CNH2 pasteurella			
RC	P57224 buchnera ap			
RC	Q7VP53 haemophilus			
RC	Q886P4 pseudomonas			
RC	Q88M11 pseudomonas			
RC	Q83BV1 coxiella bu			
RC	Q6LN23 photobacter			
RC	Q8PMP9 xanthomonas			
RC	Q8PAU5 xanthomonas			
RC	Q7QMC0 anophelles g			
RC	Q87f52 xylella fast			
RC	Q9Pf33 xylella fast			
RC	Q8D2G1 wiggleswort			
RC	Q84953 yersinia pe			
RC	Q8BCH7 pseudomonas			
RC	Q8KPV1 vibrio chol			
RC	Q82XJ5 nitrosomonas			
RC	Q62JG3 burkhodella			
RC	Q63T11 burkhodella			
RC	Q66e99 yersinia ps			
SEQUENCE FROM N. A.				
SPECIES=E.coli;				
Schramm S., Duncan M., Allen E., Araujo R., Aparicio A., Chung E., Davis K., Federpfeil N., Hyman R., Kalman S., Komp C., Kurdi O., Lashkari D., Lew H., Lin D., Namath A., Oefner P., Roberts D., Davis R.W.;				
Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.				
[15]				
SEQUENCE FROM N. A.				

OM protein - protein search, using sw model

Run on:

November 3, 2005, 08:34:05 ; Search time 40 Seconds

(without alignment)

635.031 Million cell updates/sec

Title: US-10-813-549-1

perfect score: 1380

Sequence: 1 MAISIKTPEDIEKMRVAGRL.....CEILTRKDDTIPATIHSDE 264

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database : PIR 79;*

1: pir1;*

2: pir2;*

3: pir3;*

4: pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID

Description

Result No.	Score	Query	Match	Length	DB	ID
1	1380	100.0	264	1	DBECM	
2	1380	100.0	264	2	B88501	
3	1380	100.0	254	2	B90650	
4	1258	91.2	264	2	AI0528	
5	1258	91.2	264	2	SL2027	
6	1195	86.6	263	2	AB0128	
7	937	67.9	264	2	AB4957	
8	910.5	66.0	268	2	C64138	
9	909.5	65.9	261	2	D83189	
10	852	61.7	259	2	E82845	
11	823.5	59.7	280	2	D82097	
12	795.5	57.7	261	2	AB0405	
13	758.5	55.0	259	2	E82029	
14	758.5	55.0	259	2	CB1008	
15	739	53.6	260	2	C83301	
16	723.5	52.4	256	2	AG2324	
17	697	50.5	276	2	HB1580	
18	685.5	49.7	259	2	A71642	
19	684.5	49.6	259	2	D97859	
20	669.5	48.5	253	2	S75731	
21	660	47.8	278	2	AB2774	
22	660	47.8	278	2	H91553	
23	659	47.8	276	2	A12341	
24	646	46.8	274	2	S76999	
25	634	45.9	285	2	BB7106	
26	630	45.7	285	2	T50575	
27	617	44.7	285	2	G70885	
28	594	43.0	298	2	BB8888	
29	42.9	259	2	C75410		

ALIGNMENTS

RESULT 1

DBCM

methionyl aminopeptidase (EC 3.4.11.18) (validated) - Escherichia coli (strain K-12)

N:Alternative names: metallooligopeptidase; methionine aminopeptidase; peptidase M

C:Species: Escherichia coli

C:Date: 30-Sep-1988 #sequence revision 30-Sep-1988 #text_change 09-Jul-2004

C:Accession: A27761; S45233; R67470

R:Ben-Bassat, A.; Bauer, K.; Chang, S.Y.; Myambo, K.; Boosman, A.J.; Chang, S.

J: Bacteriol. 169, 751-757, 1987

A:Title: Processing of the initiation methionine from proteins: properties of the Esche

A:Reference number: A27761; MUID:87109068; PMID:3027045

A:Accession: A27761

A:Molecule type: DNA

A:Residues: 1-264 <FUJ>

A:Cross-references: EMBL:D26562; NID:9473770; PIDN:BA05612.1; PID:9473823

A:Experimental source: strain K-12, substrain W3110

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; G.

A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A:Title: The complete genome sequence of Escherichia coli K-12.

A:Reference number: A64720; MUID:97426617; PMID:9278503

A:Accession: H64740

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-264 <BLAT>

A:Cross-references: GB:AE00126; GB:U00096; NID:91786358; PIDN: AAC73279.1; PID:91786364

A:Experimental source: strain K-12, substrain MG1655

R:Roderick, S.L.; Matthews, B.W.

B:Submitted to the Brookhaven Protein Data Bank, December 1992

A:Reference number: A51847; PDB:1MAT

A:Contents: annotation; X-ray crystallography, 2.4 angstroms, residues 2-264

R:Roderick, S.L.; Matthews, B.W.

Biochemistry, 32, 3907-3912, 1993

A:Title: Structure of the cobalt-dependent methionine aminopeptidase from Escherichia co

A:Reference number: A99470; MUID:93229487; PMID:8471602

A:Contents: annotation; X-ray crystallography, 2.4 angstroms

C:Genetics: A

C:Map: A

A:Map position: 4 min

C:Complex: monomer

C:Function: C

A:Description: catalyzes hydrolysis of amino-terminal methionine from proteins

C:Superfamily: Escherichia coli methionyl aminopeptidase

C:Keywords: aminopeptidase; cobalt; metalloprotein; monomer; protein biosynthesis

methionyl aminopeptidase (EC 3.4.11.18) (validated) - Escherichia coli (strain K-12)

methionyl aminopeptidase; metallooligopeptidase; peptidase M

N:Alternative names: metallooligopeptidase; methionine aminopeptidase; peptidase M

C:Species: Escherichia coli

C:Date: 30-Sep-1988 #sequence revision 30-Sep-1988 #text_change 09-Jul-2004

C:Accession: A27761; S45233; R67470

R:Ben-Bassat, A.; Bauer, K.; Chang, S.Y.; Myambo, K.; Boosman, A.J.; Chang, S.

J: Bacteriol. 169, 751-757, 1987

A:Title: Processing of the initiation methionine from proteins: properties of the Escherichia coli methionyl aminopeptidase

A:Reference number: A27761; MUID:87109068; PMID:3027045

A:Accession: A27761

A:Molecule type: DNA

A:Residues: 1-264 <FUJ>

A:Cross-references: EMBL:D26562; NID:9473770; PIDN:BA05612.1; PID:9473823

A:Experimental source: strain K-12, substrain W3110

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; G.

A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A:Title: The complete genome sequence of Escherichia coli K-12.

A:Reference number: A64720; MUID:97426617; PMID:9278503

A:Accession: H64740

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-264 <BLAT>

A:Cross-references: GB:AE00126; GB:U00096; NID:91786358; PIDN: AAC73279.1; PID:91786364

A:Experimental source: strain K-12, substrain MG1655

R:Roderick, S.L.; Matthews, B.W.

B:Submitted to the Brookhaven Protein Data Bank, December 1992

A:Reference number: A51847; PDB:1MAT

A:Contents: annotation; X-ray crystallography, 2.4 angstroms, residues 2-264

R:Roderick, S.L.; Matthews, B.W.

Biochemistry, 32, 3907-3912, 1993

A:Title: Structure of the cobalt-dependent methionine aminopeptidase from Escherichia coli

A:Reference number: A99470; MUID:93229487; PMID:8471602

A:Contents: annotation; X-ray crystallography, 2.4 angstroms

C:Genetics: A

C:Map: A

A:Map position: 4 min

C:Complex: monomer

C:Function: C

A:Description: catalyzes hydrolysis of amino-terminal methionine from proteins

C:Superfamily: Escherichia coli methionyl aminopeptidase

C:Keywords: aminopeptidase; cobalt; metalloprotein; monomer; protein biosynthesis

GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: November 11, 2005, 18:02:50 ; search time 2355 Seconds
(without alignments) 4267.077 Million cell updates/sec

Title: US-10-813-549-1
Perfect score: 1380

Sequence: 1 MAISIKTIEDIEKMRVAGRL.....CEILTRKDITPAIISIDE 264

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 3423954 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 6847908

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Lasting first 45 summaries

Command line parameters:
-MOBILframe+p2n.model -DEV=xlh
-Q=cgn2_1/USPTO_spool/1S10813549/runat_03112005_075935_13175/app_query.fasta_1.455
-D=EST -QFMT=FASTA -SFIXE=EST -MINMATCH=0.1 -LOOPCPC=0 -LOOPCXT=0
-UNITS=BITS -START=1 -END=1 -MATRX:blobsum62 -TRANS=human40.cdt -LIGN=45
-DOCALIGN=200 -THR SCORE=RECT -THR MAX=100 -THR MIN=0 -ALIGH=20 -MODE=LOCAL
-OUTFILE=PLC -NORM=EXT -HEAPSIZE=2000000000
-USER=US10813549 @CON 1.1 3437 @runat 03112005_075935_13175 -NCU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NIG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DBV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELEXT=6 -DELEXT=7

Database : EST*

1: gb_est1:*

2: gb_est2:*

3: gb_htc:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gss1:*

9: gb_gss2:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

§ Query Score Match Length DB ID

Result No. Description

Result No.	Score	Query Match Length	DB ID	Description
1	1351	97.9	812	9 CL661282
2	1327	96.2	844	9 CL668009
3	1236	89.6	716	9 CL663485
4	793.5	57.5	830	1 AL659413
5	786	57.0	706	8 AQ989727
6	756	54.8	839	9 CL663394
7	614	44.5	1047	9 AY420765
8	607	44.0	1335	3 CR656222
9	43.8	1047	9 AY420767	Mus muscu

10	605	43.8	2550	3 AK077694	AK077694 Mus muscu
11	604	43.8	1364	3 CR094735	CR094735 Tetraodon
12	603	43.7	870	9 C0163928	C0163928 FUDI_44_E
13	601	43.6	739	9 C1685899	C1685899 PR101425
14	599	43.4	631	8 BH762604	BH762604 BMBC330A
15	599	43.4	995	9 AY420765	AY420765 Pan trogl
16	594	43.0	1308	3 CR688406	CR688406 Tetraodon
17	585	42.4	926	3 BQ706230	BQ706230 ASENCOURT
18	578	41.9	890	7 CR458575	CR458575 922961 Ma
19	573	41.5	859	5 BQ232415	BQ232415 ASENCOURT
20	565	41.3	967	3 AR006484	AR006484 Mus muscu
21	568	41.2	940	5 BQ937757	BQ937757 ASENCOURT
22	561.5	40.7	997	7 CR264740	CR264740 EST710818
23	560.5	40.6	780	8 BZ573414	BZ573414 mbh2_3093
24	558.5	40.5	867	7 CF205959	CF205959 RIB909151
25	558.5	40.5	888	7 CN159313	CN159313 CIBud005
26	556.5	40.3	1235	7 CR514702	CR514702 ABridops
27	549.5	39.8	876	5 BII36049	BII36049 633124836
28	548.5	39.7	1278	3 CNS02A284	BX827791 Arabidops
29	547	39.6	742	4 BU434305	BU434305 BU434177
30	547	39.6	760	4 BU432212	BU432212 BU432312
31	545	39.5	888	7 CN159313	CN159313 948372 MA
32	542.5	39.3	637	1 AUT22058	AUT22058 AY72958
33	542.5	39.3	818	7 CO978666	CO978666 GH90052A1
34	541	39.2	682	6 CDD17720	CDD17720 VIB142009
35	541	39.2	761	4 BU434187	BU434187 BU434187
36	540.5	39.2	1347	8 BZ554793	BZ554793 Pacs1-60
37	537.5	38.9	915	7 CK269489	CK269489 EST715567
38	533	38.6	778	7 CN35924	CN35924 9159113
39	532.5	38.6	898	7 CV23178	CV23178 17000562
40	530.5	38.4	989	7 CO25282	CO25282 WS25188.B
41	528	38.3	715	4 BU435572	BU435572 BB463358
42	527.5	38.2	684	2 BB463358	BB463358 BB468358
43	527.5	38.2	797	2 BE902721	BE902721 60167531
44	526	38.1	722	2 CA229368	CA229368 SCBFF507
45	526	38.1	731	1 AV881422	AV881422 AV881422

ALIGNMENTS

RESULT 1

CL661282

DEFINITION

CL661282

ACCESION

CL661282.1

VERSION

GI:50147601

KEYWORDS

CSS.

SOURCE

Pristionchus pacificus

ORGANISM

Pristionchus pacificus

REFERENCE

1 (bases 1 to 812)

AUTHORS

Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.

TITLE

AppDB: an AcedB database for the nematode satellite organism

JOURNAL

Nucleic Acids Res. 32 (1), D421-D422 (2004)

COMMENT

Evolutionary Biology

Max-Planck-Institute for Developmental Biology

Spemannstr. 37-39, Tuebingen D-72076, Germany

Tel: 00497071601371

Fax: 00497071601498

Email: ralf.sommer@uebingen.mpg.de

This library was generated at Caltech, Pasadena, USA and end sequenced at Vancouver, Canada.

Seq Primer: T7

Class: fowlid ends.

Location/Qualifiers

.812

/organism="Pristionchus pacificus"

/mol_type="genomic DNA"

Om protein - nucleic search, using frame_plus_p2n model

Run on: November 11, 2005, 16:26:32 ; Search time 3123 Seconds

(without alignments) 4096.118 Million coll updates/sec

Title: US-10-813-549-1

Perfect score: 1380

Sequence: 1 MAISIKTPEDIKEKVRAGRL..... CELITLRKDTIPAIISHDE 264

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries:

Command line parameters:
 -MOBL=frame+p2n.model -DEV=x1h
 -Q=cgn2.1/USPRO spool/US10813549/runat_03112005_075935_13164/app_query.fasta_1.455
 -DB=GenBml -QFORMAT=Fastaa -SUFFIX=arg -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40 cdi -LIST=45
 -DOCALLIGR=200 -THR_SCORE=PCT -THR_MAX=100 -THR_MIN=0 -ALIGN=20 -MODE=LOCAL
 -OUTFMT=pto -NORM=ext -THRESHOLD=500 -MINLEN=0 -MAXLEN=0000000000
 -USR=USR10813549 @CGN 1 1 3731 @runat 0112005 075935_13164 -NCPU=6 -ICPU=3
 -NO_MMAPP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSBLOCK=10 -LONGLOG
 -DET_TIMEOUT=20 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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1: GenBml:*
2: gb_ba:*
3: gb_tntg:*
4: gb_in:*
5: gb_on:*
6: gb_bt:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

```

RESULT 1

ECOMAP ECOMAP
 LOCUS ECOMAP
 DEFINITION E.coli map gene, encoding methionine amino peptidase, complete cds.
 ACCESSION M15106
 VERSION M15106.1 GI:146726
 KEYWORDS map gene; metallo-oligopeptidase; methionine aminopeptidase.
 SOURCE Escherichia coli
 ORGANISM Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.
 REFERENCE 1 (base 1 to 1197)
 AUTHORS Ben-Bassat,A., Bauer,K., Chang,S.Y., Myambo,K., Boosman,A. and Chang,S.
 TITLE processing of the initiation methionine from proteins: properties of the Escherichia coli methionine aminopeptidase and its gene structure
 J. Bacteriol. 169 (2), 751-757 (1987)
 JOURNAL 8710966
 MEDLINE 3027045
 PUBMED
 COMMENT Original source text: E.coli (strain CM89) DNA, clone PSY174. Draft entry and computer-readable sequence for [1] kindly provided by S.Chang, 01-JUN-1987.
 There are at least two tandem 'map' gene promoters separated by the Small Site at position 150. Two regions of dyad symmetry are located at positions 187-201 and 1018-1037. 1. .1197
 FEATURES Source
 1. .1197

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match Length	DB ID	Description
1	1380	100.0	1197	1 BCOMAP
2	1380	100.0	1197	6 E01194
3	1380	100.0	1197	6 I02088
4	1380	100.0	1197	6 I02543

OM protein - nucleic search, using frame_plus_p2n model

Run on:

November 11, 2005, 18:29:14 ; Search time 621 seconds

(without alignments) 315.67 Million cell updates/sec

SUMMARIES

Title: US-10-813-549-1
Perfect score: 1380
Sequence: 1 MAISIKTIPEDIEKMRVAGRL.....CBILTRKDDTIPAIISHDE 264

Scoring table: BLOSUM62

Xgapop 10.0 Xgapext 0.5
 Ygapop 10.0 Ygapext 0.5
 Fgapop 6.0 Fgapext 7.0
 Delop 6.0 Delext 7.0

Searched: 9794790 seqs, 4134909557 residues

Total number of hits satisfying chosen parameters: 19589580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Command line parameters:

-MODE:frame+ p2n.model -DEV=xlh
 -O=/cgn2_1/USPTO_spool/US103549/runat_03112005_075936_13214/app_query.fasta_1.455
 -Db=Published_Applications_NA -QWRT=fastap -SUFFIX=impb -MINMATCH=0.1
 -LOOPCL=0 -LOOPEXTN=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
 -TRANS=human40_cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=pcit -THR MAX=100
 -THR MIN=0 -ALIGN=20 -NODE=LOCAL -OUTFILE=pro -NORM=next -HEAPSIZE=500 -MINLEN=0
 -MAXLEN=200000000 -USER=US1081549 -GCN 1 1 480 @runat 03112005_075936_13214
 -NCPU=6 -ICLU=3 -NO_MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
 -LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
 -FGAPOP=6 -FGAPEXT=7 -YGAPO=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

1: Published_Applications_NA,*
 2: /cgn2_6/ptodata/1/pubpna/us07_PUBCOMB.seq,*
 3: /cgn2_6/ptodata/1/pubpna/us06_NEW_PUB.seq,*
 4: /cgn2_6/ptodata/1/pubpna/us06_PUBCOMB.seq,*
 5: /cgn2_6/ptodata/1/pubpna/us07_NEW_PUB.seq,*
 6: /cgn2_6/ptodata/1/pubpna/PCUTUS_PUBCOMB.seq,*
 7: /cgn2_6/ptodata/1/pubpna/us08_NEW_PUB.seq,*
 8: /cgn2_6/ptodata/1/pubpna/us08_PUBCOMB.seq,*
 9: /cgn2_6/ptodata/1/pubpna/us09A_PUBCOMB.seq,*
 10: /cgn2_6/ptodata/1/pubpna/us09B_PUBCOMB.seq,*
 11: /cgn2_6/ptodata/1/pubpna/us09C_PUBCOMB.seq,*
 12: /cgn2_6/ptodata/1/pubpna/us09_NEW_PUB.seq,*
 13: /cgn2_6/ptodata/1/pubpna/us10_NEW_PUB.seq,*
 14: /cgn2_6/ptodata/1/pubpna/us10_PUBCOMB.seq,*
 15: /cgn2_6/ptodata/1/pubpna/us10B_PUBCOMB.seq,*
 16: /cgn2_6/ptodata/1/pubpna/us10C_PUBCOMB.seq,*
 17: /cgn2_6/ptodata/1/pubpna/us10H_PUBCOMB.seq,*
 18: /cgn2_6/ptodata/1/pubpna/us10E_PUBCOMB.seq,*
 19: /cgn2_6/ptodata/1/pubpna/us10F_PUBCOMB.seq,*
 20: /cgn2_6/ptodata/1/pubpna/us10G_PUBCOMB.seq,*
 21: /cgn2_6/ptodata/1/pubpna/us10H_PUBCOMB.seq,*
 22: /cgn2_6/ptodata/1/pubpna/us10I_PUBCOMB.seq,*
 23: /cgn2_6/ptodata/1/pubpna/us10J_PUBCOMB.seq,*
 24: /cgn2_6/ptodata/1/pubpna/us10_NEW_PUB.seq,*
 25: /cgn2_6/ptodata/1/pubpna/us11A_PUBCOMB.seq,*
 26: /cgn2_6/ptodata/1/pubpna/us11_NEW_PUB.seq,*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

Result No.	Score	Query Match Length	DB ID	Description
SUMMARIES				
c 1	1380	100.0	11204	22 US-10-893-671-30
c 2	937	67.9	640681	9 US-09-790-988-1
c 3	911.5	66.1	908766	24 US-10-795-159-685
c 4	910.5	66.0	807	24 US-10-958-216-120
c 5	910.5	66.0	1830121	18 US-10-328-670-1
c 6	910.5	66.0	1830121	21 US-10-188-865-1
c 7	910.5	66.0	1830121	24 US-10-981-687-1
c 8	909.5	65.9	786	24 US-10-958-216-58
c 9	909.5	65.9	786	24 US-10-958-216-60
c 10	904.5	65.5	807	24 US-10-958-216-122
c 11	852	61.7	2731748	20 US-10-297-465A-1
c 12	799.5	57.9	96109	19 US-10-672-787-35
c 13	758.5	55.0	92934	24 US-10-915-740B-01
c 14	758.5	55.0	2242716	24 US-10-915-740B-1068
c 15	619	44.9	855	16 US-10-116-761-5908
c 16	619	44.9	9025608	16
c 17	617.5	44.7	1735	21 US-10-425-115-114629
c 18	614	44.5	2671	18 US-10-239-867-1
c 19	614	44.5	2671	21 US-10-733-860-1102
c 20	614	44.5	2984	18 US-10-339-645-28
c 21	597.5	43.3	330940	9 US-09-738-626-1
c 22	595	43.1	1125	26 US-11-097-143-31928
c 23	594	43.0	1197	9 US-09-938-842A-2427
c 24	594	43.0	1197	11 US-09-938-842A-427
c 25	590	42.8	747	9 US-09-974-300-1195
c 26	590	42.8	1747	24 US-10-510-812-33
c 27	590	42.8	1747	19 US-10-524-599-104571
c 28	587	42.5	1605	116 17 US-10-032-585-6897
c 29	574.5	41.6	1116	17 US-10-117-143-3124
c 30	571.5	41.4	2287	26 US-11-971-143-3127
c 31	571.5	41.4	3252	26 US-11-971-143-3127
c 32	565.5	41.0	1360	21 US-10-425-115-452
c 33	562.5	40.8	1295	19 US-10-325-114-26339
c 34	557.5	40.4	1306	20 US-10-337-963-48339
c 35	552.5	40.0	3088	21 US-10-723-860-5641
c 36	550.5	39.9	1534	19 US-10-124-599-30704
c 37	550.5	39.9	1534	19 US-10-125-168-772
c 38	547.5	39.7	1389	20 US-10-425-168-772
c 39	539	39.1	120025	18 US-10-437-963-68096
c 40	531.5	38.9	389	18 US-10-424-599-762-1
c 41	519	37.6	762	24 US-10-958-216-102
c 42	519	37.6	1856	9 US-09-070-92A-494
c 43	518.5	37.6	943	10 US-11-097-143-10796
c 44	518.5	37.6	1734	21 US-10-425-115-14723
c 45	516	37.4	807	24 US-10-501-282-3477

ALIGNMENTS

RESULT 1				
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				; Sequence 30, Application US/10893671
				; Publication No. US2005064527A1
				; GENERAL INFORMATION:
				; APPLICANT: LEVY, STUART, et al.
				; TITLE OF INVENTION: NMR COMPOSITIONS AND THEIR METHODS OF USE
				; FILE REFERENCE: PZZ-043
				; CURRENT APPLICATION NUMBER: US/10-893, 671
				; CURRENT FILING DATE: 2004-07-15
				; PRIOR APPLICATION NUMBER: US/09/801, 563
				; PRIOR FILING DATE: 2001-03-08
				; PRIOR APPLICATION NUMBER: 60/188, 362
				; PRIOR FILING DATE: 2000-03-10

